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SEQUENCE HEOTSDSD

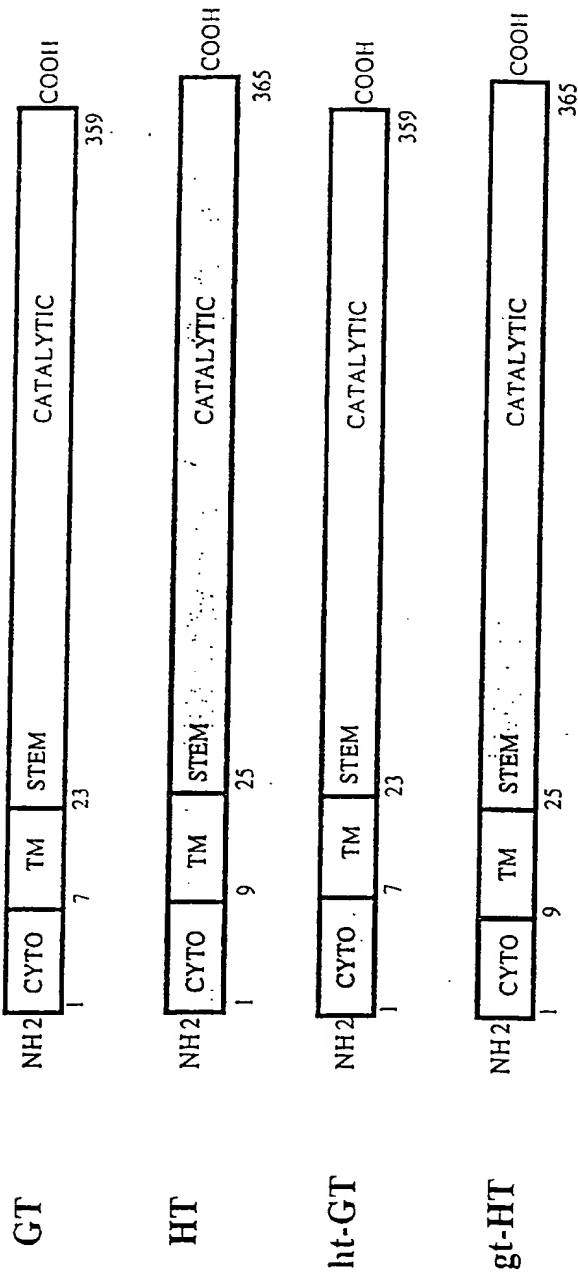


FIGURE 1

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Sign

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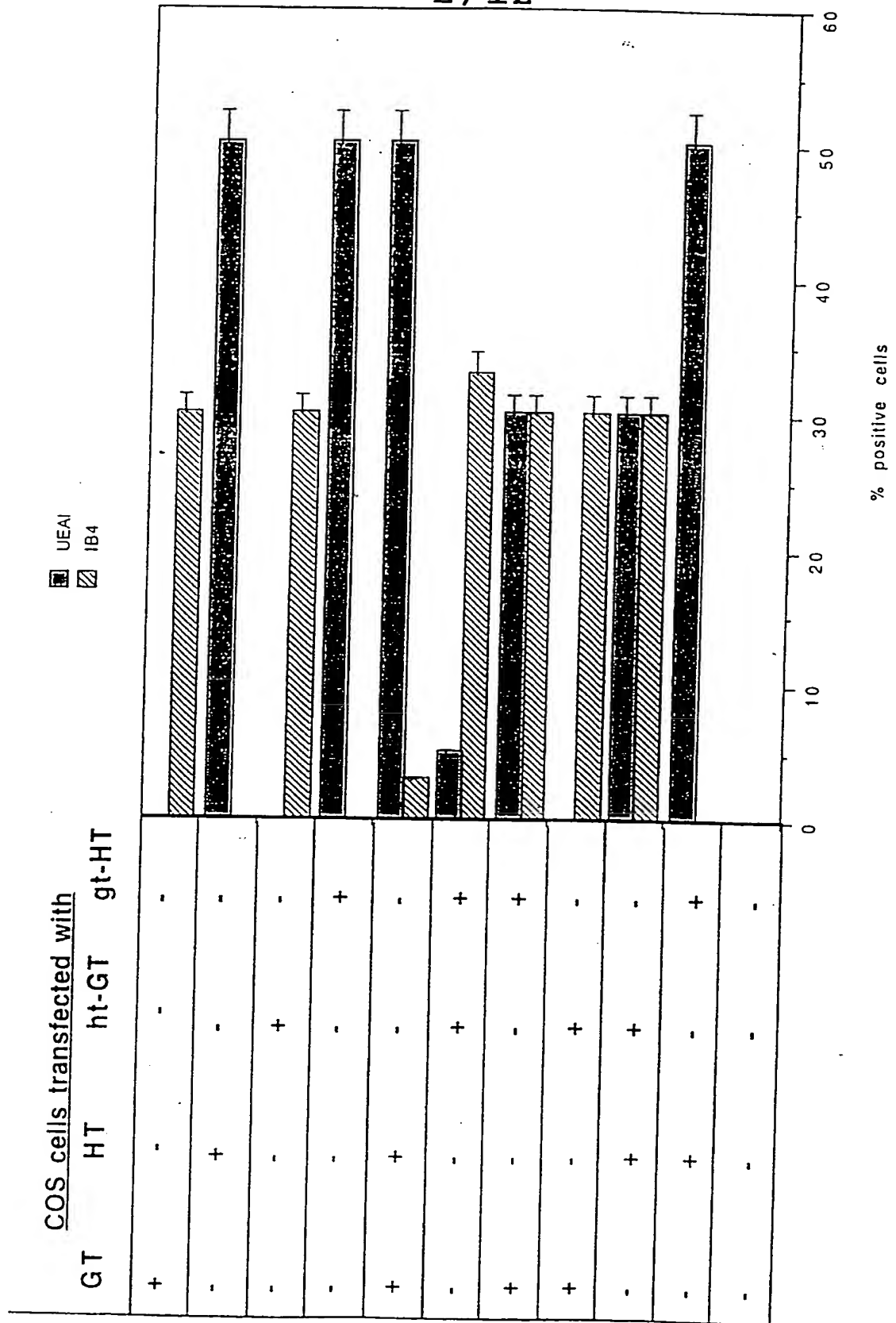


FIGURE 2

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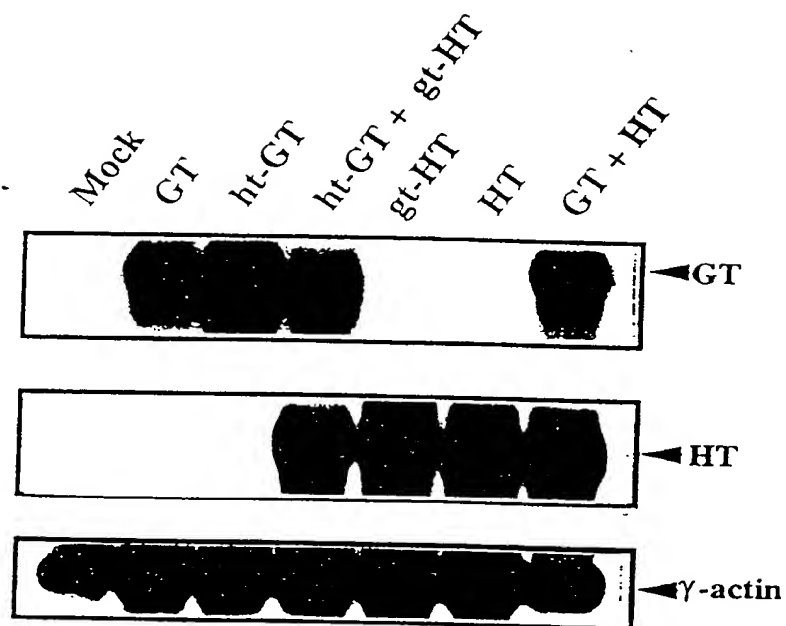


FIGURE 3

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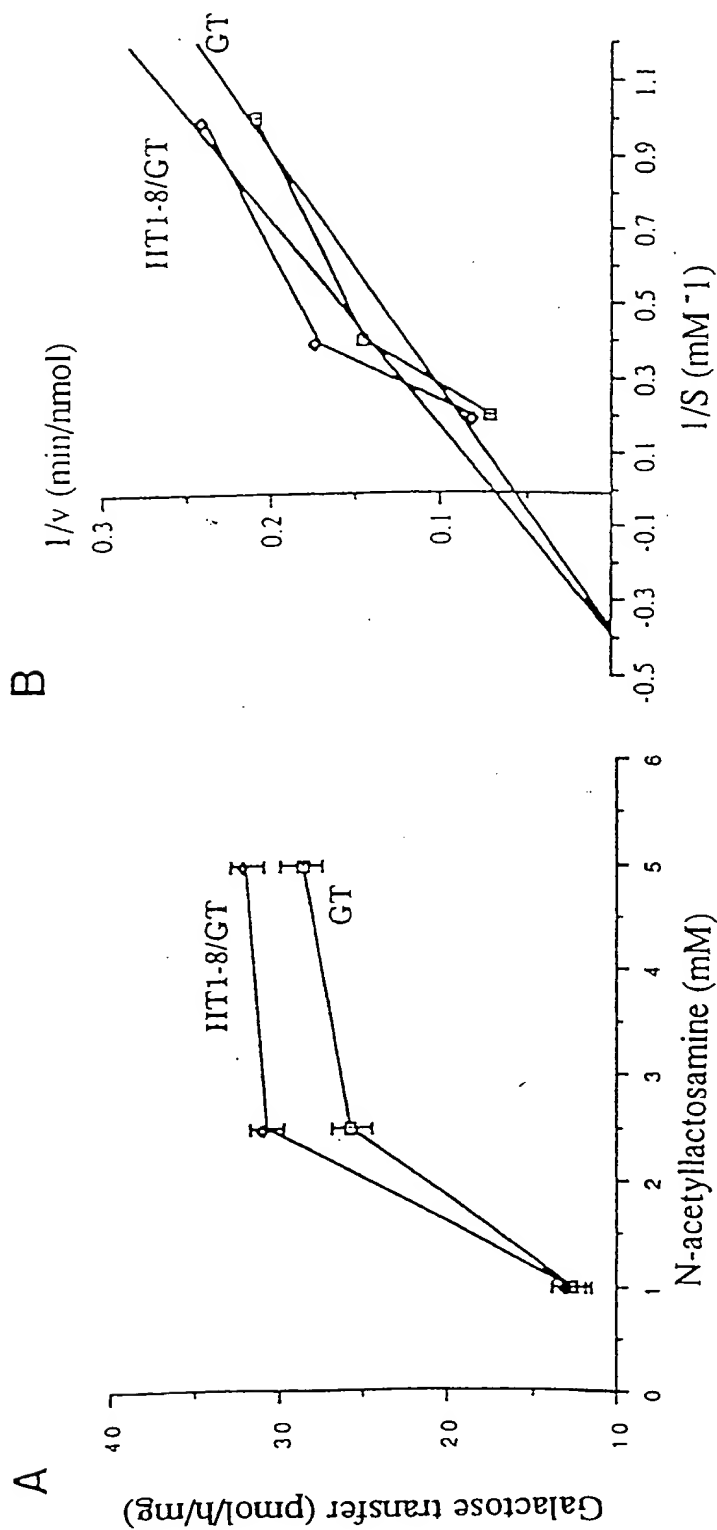


FIGURE 4

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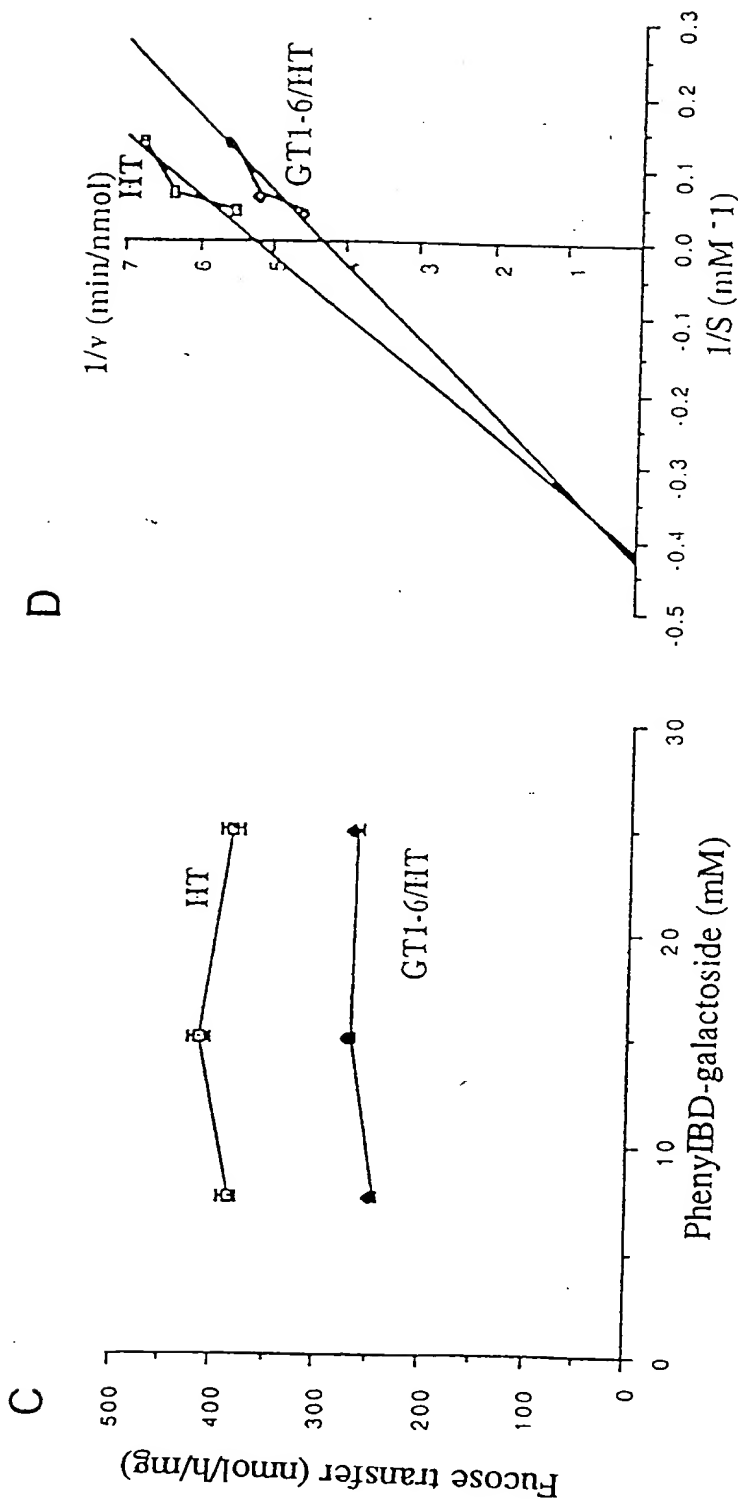


FIGURE 4 Continued

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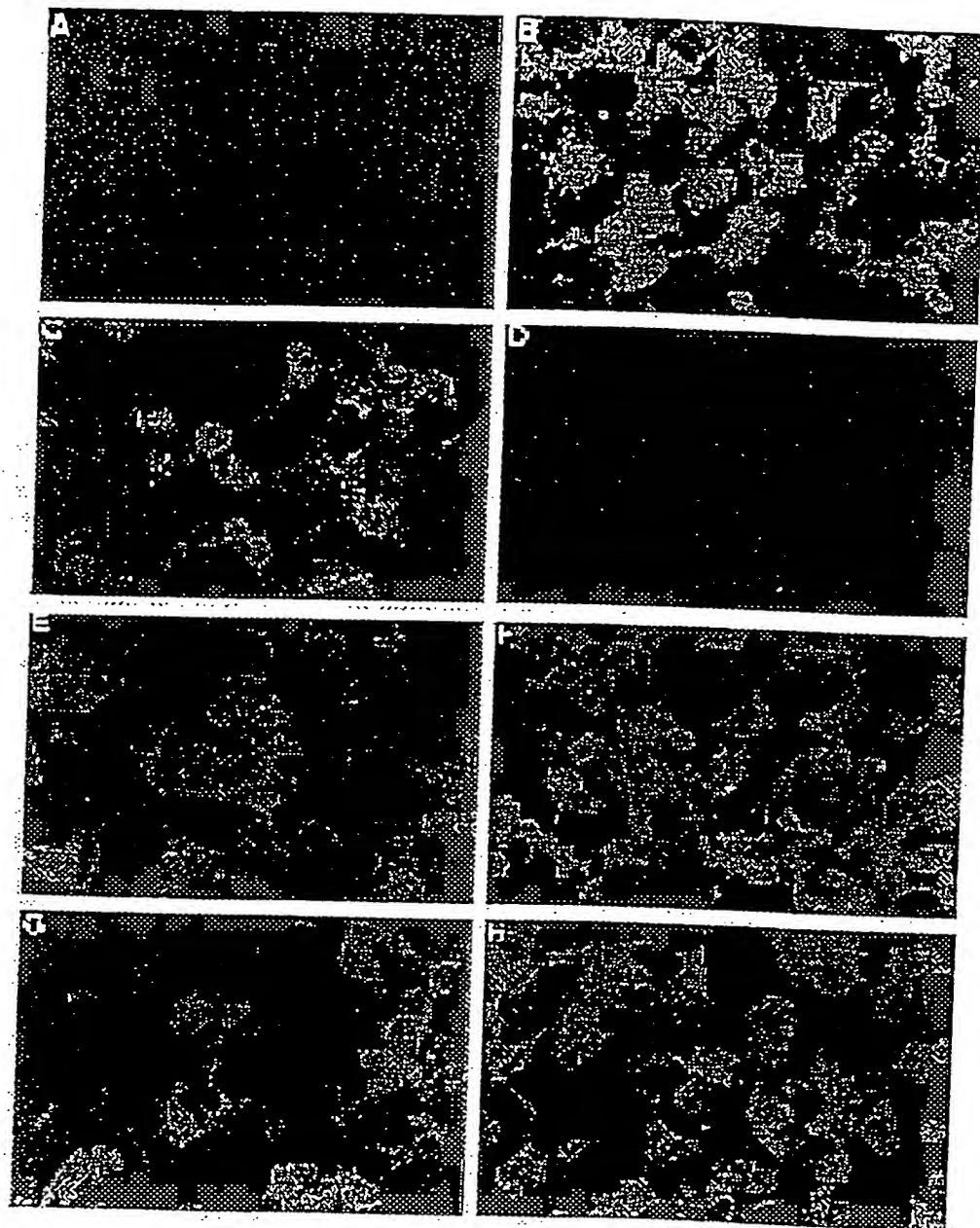


FIGURE 5

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PORCINE SECRETOR SEQUENCE

M L S M Q A S F F P T G P F I L 17
CT ACA GCC ATG CTC AGC ATG CAG GCA TCC TTC TTC CCC ACG GGT CCC TTC ATC CTC 59
F V F T A S T I F H L Q Q R H V K I Q P 37
TTT GTC TTC ACG GCT TCC ACC ATA TTT CAC CAG CAG AGG ATG GTG AAG ATT CAA CCC 119
T W E L Q M V T Q V T T E S P S S P Q L 57
ACG TGG GAG TTA CAG ATG GTG ACG CAG GTG ACC ACA GAG AGC CCC TCG AGC CCC CAG CTG 179

PORCINE SECRETOR SEQUENCE

K G M W T I N A I G R L G N Q M G E Y A 77
AAG GGC ATG TGG ACG ATC AAT GCC ATC GGC CGC CTG GGG AAC CAG ATG GGG GAG TAC GCC 239
T L Y A L A R M N G R P A F I P P E M H 97
ACC CTG TAC GCG CTG GCC AGG ATG AAC GGC CGG CCG GCC TTC ATC CCG CCC GAG ATG CAC 299
S T L A P I F R I T L L P V L H A S T A R 117
AGC ACG CTG GCC CCC ATC TTC AGG ATC ACC CTC CCG GTC CTG CAC GCC AGC ACG GCC CGC 359
R I P W Q N Y H L N D W M E E R Y R H I 137
AGG ATC CCC TGG CAG AAC TAC CAC CTG AAC GAC TGG ATG GAG CAG CGG TAC CGC CAC ATC 419
P G E Y V R L T G Y P C S W T F Y H L 157

FIGURE 6

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SEQUENCE "HEOTSDSD"

CCG GGG GAG TAC GTG CGC CTC ACG GGC TAC CCC TGC TCC TGG ACC TTC TAC CAC CAC CTG 479
 R T E I L R E F T L H N H V R E E A Q D 177
 CGC ACC GAG ATC CTC CGG GAG TTC ACC CTG CAT AAC CAC GTG CGC GAG GAG GCC CAG GAT 539
 F L R G L R V N G S R P S T Y V G V H V 197
 TTC CTG CGG GGT CTG CGG GTG AAC GGG AGC CGA CCG AGT ACC TAC GTG GGG GTG CAC GTG 599
 R R G D Y V H V M P N V W K G V V A D R 217
 CGC CGG GGG GAC TAC GTG CAC GTG ATG CCC AAC GTG TGG AAG GGC GTG GTG GCC GAC CGG 659
 R Y L E Q A L D W F R A R Y R S P V F V 237
 CGG TAC CTG GAG CAG GCC CTG GAC TGG TTC CGG GCT CGC TAC CGC TCC CCC GTC TTT GTG 719
 V S S N G M A W C R E N I N A S R G D V 257
 GTC TCC AGC AAC GGC ATG GCC TGG TGT CGG GAA AAC ATC AAT GCC TCG CGC GGC GAT GTG 779
 V F A G N G I E G S P A K D F A L L T Q 277
 GTG TTT GCC GGC AAT GGC ATC GAG GGC TCC CCC GCC AAA GAC TTC GCG CTG CTC ACG CAG 839
 C N H T V M T I G T F G I W A A Y L A G 297
 TGT AAC CAC ACT GTC ATG ACC ATT GGC ACG TTC GGG ATC TGG GCC TAC CTT GCT GGT 899
 G E T I Y L A N Y T L P D S P F L K L F 317
 GGA GAG ACC ATC TAC CTG GCC AAT TAC ACG CTC CCG GAC TCT CCC TTC CTC AAA CTC TTT 959

FIGURE 6 (cont.)

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K	P	E	A	A	F	L	P	E	W	I	G	I	E	A	D	L	S	P	L	337
AAG	CCC	GAG	GCA	GCC	TTC	CTG	CCC	GAG	TGG	ATT	GGG	ATC	GAG	GCA	GAC	CTG	TCC	CCA	CTC	1019
L	K	H	*													340				
CTT	AAG	CAC	TGA	TGT	CGG	CTG	TCC													1043

FIGURE 6 (cont.)

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PIG H TRANSFERASE

M W V P S R R H L C L T F L - L V C V L A	20
ATGTGGGTCCCCAGCCGCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTATGCA	60
A T F F L N V Y Q D L F Y S G L D L L A	40
GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGSCC	120
L C P D H N V V S S P V A I F C L A G T	60
CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCACC	180
P V H P N A S D S C P K H P A S F S G T	80
CCGSTACACCCCAACGCCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC	240
W T I Y P D G R F G N Q M G Q Y A T L L	100
TGGACTATTTACCCGGATGGCCGGTTTGGGAACAGATGGGACAGTATGCCACGCTGCTG	300
A L A Q L N G R Q A F I Q P A M H A V L	120
GCCCTGGCGCAGCTCAACGGCGCCAGGCGCTTCATCCAGCCTGCCATGCACGCCGCTCCTG	360
A P V F P R I T L P V L A P E V D R H A P	140
CCCCCGGTGTTCCGCATCAGGCTGCCTGTCTGCGCGCCGAGGTAGACAGGCACGCTCCT	420
W R E L E L H D W M S E D Y A H L K E P	160
TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC	480
W L K L T G F P C S W T F F H H L R E Q	180
TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG	540
I R S E F T L H D H L R Q E A Q G V L S	200
ATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGGCCAGGGGGTACTGAGT	600
Q F R L P R T G D R P S T F V G V H V R	220
CAGTTCGCTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC	660
R G D Y L R V M P K R W K G V V G D G A	240
CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT	720
Y L Q Q A N D W F R A R Y E A P V F V V	260
TACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC	780
T S N G M E W C R K N I D T S R G D V I	280
ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC	840
F A G D G R E A A P A R D F A L L V Q C	300
TTTGCTGGCGATGGGCGGGAGGCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC	900
N H T I M T I G T F G F W A A Y L A G G	320
AACCACACCATCATGACCATTTGGCACCTTCGGCTTCTGGGCCGCTACCTGGCTGGTGGA	960
D T I Y L A N F T L P T S S F L K I F K	340
GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTCTGAAGATCTTTAA	1020
P E A A F L P E W V G I N A D L S P L Q	360
CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG	1080
M L A G P	365
ATGTTGGCTGGGCCTTGA	1093

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FIGURE 7

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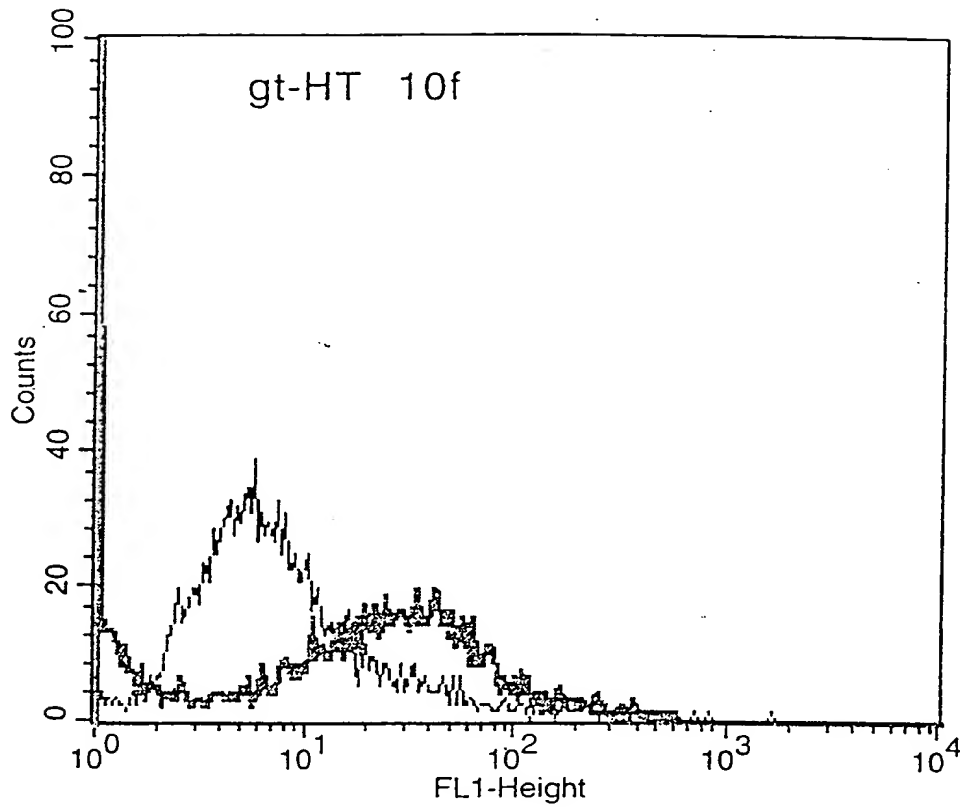


FIGURE 8

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FIGURE 9

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